

## SEQUENCE LISTING

&lt;110&gt; RIKEN

<120> Transgenic plants carrying neoxanthin  
cleavage enzyme gene

&lt;130&gt; R3-102DP1

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; JP 2000-010056

&lt;151&gt; 2000-01-13

&lt;160&gt; 32

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1752

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1752)

&lt;400&gt; 1

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atg gtt tct ctt ctt aca atg ccg atg agt ggt ggt att aaa aca tgg 48
Met Val Ser Leu Leu Thr Met Pro Met Ser Gly Gly Ile Lys Thr Trp
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cct caa gcc caa att gat ttg ggt ttt agg ccc att aaa aga caa ccg 96
Pro Gln Ala Gln Ile Asp Leu Gly Phe Arg Pro Ile Lys Arg Gln Pro
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aag gtt att aaa tgc acg gtg cag atc gac gta acg gaa tta acc aaa 144
Lys Val Ile Lys Cys Thr Val Gln Ile Asp Val Thr Glu Leu Thr Lys
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aaa cgc caa tta ttt aca ccc aga acc acc gct act ccg ccg cag cat 192  
 Lys Arg Gln Leu Phe Thr Pro Arg Thr Thr Ala Thr Pro Pro Gln His  
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aat cct ctc cgg cta aac atc ttc cag aaa gcg gcg gcg att gcg atc 240  
 Asn Pro Leu Arg Leu Asn Ile Phe Gln Lys Ala Ala Ala Ile Ala Ile  
 65 70 75 80

gac gcg gct gag cgt gca tta atc tca cac gag caa gat tct cca ctt 288  
 Asp Ala Ala Glu Arg Ala Leu Ile Ser His Glu Gln Asp Ser Pro Leu  
 85 90 95

ccc aaa acc gct gat cca cgt gtt cag att gcc ggg aat tat tcc ccg 336  
 Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Tyr Ser Pro  
 100 105 110

gta ccg gaa tct tcc gtc cgg cga aac ctc acc gtc gaa gga aca atc 384  
 Val Pro Glu Ser Ser Val Arg Arg Asn Leu Thr Val Glu Gly Thr Ile  
 115 120 125

cct gac tgc att gac ggt gtt tat atc cgt aac ggc gcg aat ccg atg 432  
 Pro Asp Cys Ile Asp Gly Val Tyr Ile Arg Asn Gly Ala Asn Pro Met  
 130 135 140

ttt gag cca aca gct ggg cac cat tta ttc gac gga gac gga atg gtt 480  
 Phe Glu Pro Thr Ala Gly His His Leu Phe Asp Gly Asp Gly Met Val  
 145 150 155 160

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 His Ala Val Lys Ile Thr Asn Gly Ser Ala Ser Tyr Ala Cys Arg Phe  
 165 170 175

aca aaa acc gag aga ttg gtt cag gaa aaa cga ttg ggt cga cca gtt 576  
 Thr Lys Thr Glu Arg Leu Val Gln Glu Lys Arg Leu Gly Arg Pro Val  
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 Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile Ala Arg  
 195 200 205

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 2021-2022  
 2023-2024  
 2025-2026  
 2027-2028  
 2029-2030

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 Leu Met Leu Phe Tyr Ala Arg Gly Leu Cys Gly Leu Ile Asn Asn Gln  
 210 215 220

aac ggc gtc gga gta gca aac gcc ggt ttg gtt tac ttt aat aac cgg 720  
 Asn Gly Val Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Asn Arg  
 225 230 235 240

ctt tta gct atg tca gaa gac gat tta ccg tac caa tta aaa att act 768  
 Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr Gln Leu Lys Ile Thr  
 245 250 255

caa acc ggc gat ctc caa acc gtt gga cgt tac gat ttc gac ggt cag 816  
 Gln Thr Gly Asp Leu Gln Thr Val Gly Arg Tyr Asp Phe Asp Gly Gln  
 260 265 270

tta aaa tcc gca atg ata gct cac ccg aaa ctg gac ccg gtt acg aag 864  
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 275 280 285

gag ctt cac gcg tta agc tac gac gtc gtt aag aaa cct tac ctg aaa 912  
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tac ttc aga ttc tcg cca gac ggc gtt aaa tcg ccg gaa ttg gag atc 960  
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 305 310 315 320

ccg ctc gaa act ccg acg atg att cac gat ttc gct ata acg gag aat 1008  
 Pro Leu Glu Thr Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn  
 325 330 335

ttt gtg gtg att cct gat caa caa gtc gtg ttc aag ctc ggc gag atg 1056  
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 340 345 350

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ttg ggg ata atg ccc aag gac gcg aca gaa gct tct cag ata atc tgg 1152  
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 370 375 380

gtg aac tct ccg gag acg ttc tgt ttt cat ctc tgg aat gca tgg gaa 1200  
 Val Asn Ser Pro Glu Thr Phe Cys Phe His Leu Trp Asn Ala Trp Glu  
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tcg ccg gag acg gag gag att gtg gtg atc gga tgc tgt atg tgc ccg 1248  
 Ser Pro Glu Thr Glu Glu Ile Val Val Ile Gly Ser Cys Met Ser Pro  
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gcg gat tca atc ttc aac gag aga gac gag agc ttg aga agc gtt ttg 1296  
 Ala Asp Ser Ile Phe Asn Glu Arg Asp Glu Ser Leu Arg Ser Val Leu  
 420 425 430

tcg gag atc agg ata aac ctc aga aca cgt aaa acc acg cgt cgt tgc 1344  
 Ser Glu Ile Arg Ile Asn Leu Arg Thr Arg Lys Thr Thr Arg Arg Ser  
 435 440 445

ttg ttg gtt aac gag gat gta aat tta gag att ggt atg gtt aac cgg 1392  
 Leu Leu Val Asn Glu Asp Val Asn Leu Glu Ile Gly Met Val Asn Arg  
 450 455 460

aac cgg tta gga aga aaa acc cgg ttc gcg ttt ttg gct att gct tat 1440  
 Asn Arg Leu Gly Arg Lys Thr Arg Phe Ala Phe Leu Ala Ile Ala Tyr  
 465 470 475 480

cct tgg cca aaa gtt tcc ggt ttc gct aag gtc gat ctt tgc acc ggt 1488  
 Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Cys Thr Gly  
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gag atg aaa aaa tat att tac ggc ggt gag aaa tat ggc ggc gaa ccg 1536  
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 500 505 510

ttt ttc ttg ccc ggc aac tcc ggt aac ggc gaa gaa aat gaa gat gac 1584  
 Phe Phe Leu Pro Gly Asn Ser Gly Asn Gly Glu Glu Asn Glu Asp Asp  
 515 520 525

ggt tat ata ttt tgt cac gtt cat gac gaa gaa aca aag aca tca gag 1632  
 Gly Tyr Ile Phe Cys His Val His Asp Glu Glu Thr Lys Thr Ser Glu  
           530                          535                          540

ctt cag att att aac gct gtt aat tta aag ctt gaa gct acg att aaa 1680  
 Leu Gln Ile Ile Asn Ala Val Asn Leu Lys Leu Glu Ala Thr Ile Lys  
           545                          550                          555                          560

cta ccg tct aga gta ccg tat ggg ttt cat ggc aca ttt gtg gat tcg 1728  
 Leu Pro Ser Arg Val Pro Tyr Gly Phe His Gly Thr Phe Val Asp Ser  
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aat gaa ctc gtt gat caa tta taa 1752  
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<211> 583

<212> PRT

<213> Arabidopsis thaliana

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                           20                          25                          30

Lys Val Ile Lys Cys Thr Val Gln Ile Asp Val Thr Glu Leu Thr Lys  
           35                          40                          45

Lys Arg Gln Leu Phe Thr Pro Arg Thr Thr Ala Thr Pro Pro Gln His  
           50                          55                          60

Asn Pro Leu Arg Leu Asn Ile Phe Gln Lys Ala Ala Ala Ile Ala Ile  
       65                          70                          75                          80

Asp Ala Ala Glu Arg Ala Leu Ile Ser His Glu Gln Asp Ser Pro Leu

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85					90					95						
Pro	Lys	Thr	Ala	Asp	Pro	Arg	Val	Gln	Ile	Ala	Gly	Asn	Tyr	Ser	Pro	
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Val	Pro	Glu	Ser	Ser	Val	Arg	Arg	Asn	Leu	Thr	Val	Glu	Gly	Thr	Ile	
115					120					125						
Pro	Asp	Cys	Ile	Asp	Gly	Val	Tyr	Ile	Arg	Asn	Gly	Ala	Asn	Pro	Met	
130					135					140						
Phe	Glu	Pro	Thr	Ala	Gly	His	His	Leu	Phe	Asp	Gly	Asp	Gly	Met	Val	
145					150					155					160	
His	Ala	Val	Lys	Ile	Thr	Asn	Gly	Ser	Ala	Ser	Tyr	Ala	Cys	Arg	Phe	
165					170					175						
Thr	Lys	Thr	Glu	Arg	Leu	Val	Gln	Glu	Lys	Arg	Leu	Gly	Arg	Pro	Val	
180					185					190						
Phe	Pro	Lys	Ala	Ile	Gly	Glu	Leu	His	Gly	His	Ser	Gly	Ile	Ala	Arg	
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Leu	Met	Leu	Phe	Tyr	Ala	Arg	Gly	Leu	Cys	Gly	Leu	Ile	Asn	Asn	Gln	
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Asn	Gly	Val	Gly	Val	Ala	Asn	Ala	Gly	Leu	Val	Tyr	Phe	Asn	Asn	Arg	
225					230					235					240	
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245					250					255						
Gln	Thr	Gly	Asp	Leu	Gln	Thr	Val	Gly	Arg	Tyr	Asp	Phe	Asp	Gly	Gln	
260					265					270						
Leu	Lys	Ser	Ala	Met	Ile	Ala	His	Pro	Lys	Leu	Asp	Pro	Val	Thr	Lys	
275					280					285						
Glu	Leu	His	Ala	Leu	Ser	Tyr	Asp	Val	Val	Lys	Lys	Pro	Tyr	Leu	Lys	
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Tyr Phe Arg Phe Ser Pro Asp Gly Val Lys Ser Pro Glu Leu Glu Ile  
305 310 315 320

Pro Leu Glu Thr Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn  
325 330 335

Phe Val Val Ile Pro Asp Gln Gln Val Val Phe Lys Leu Gly Glu Met  
340 345 350

Ile Ser Gly Lys Ser Pro Val Val Phe Asp Gly Glu Lys Val Ser Arg  
355 360 365

Leu Gly Ile Met Pro Lys Asp Ala Thr Glu Ala Ser Gln Ile Ile Trp  
370 375 380

Val Asn Ser Pro Glu Thr Phe Cys Phe His Leu Trp Asn Ala Trp Glu  
385 390 395 400

Ser Pro Glu Thr Glu Glu Ile Val Val Ile Gly Ser Cys Met Ser Pro  
405 410 415

Ala Asp Ser Ile Phe Asn Glu Arg Asp Glu Ser Leu Arg Ser Val Leu  
420 425 430

Ser Glu Ile Arg Ile Asn Leu Arg Thr Arg Lys Thr Thr Arg Arg Ser  
435 440 445

Leu Leu Val Asn Glu Asp Val Asn Leu Glu Ile Gly Met Val Asn Arg  
450 455 460

Asn Arg Leu Gly Arg Lys Thr Arg Phe Ala Phe Leu Ala Ile Ala Tyr  
465 470 475 480

Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Cys Thr Gly  
485 490 495

Glu Met Lys Lys Tyr Ile Tyr Gly Gly Glu Lys Tyr Gly Gly Glu Pro  
500 505 510

09758369-047001

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Asp Asn Asn Asp Arg Arg Asn Lys Pro Lys Thr Leu His Asn Arg Thr



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aat cac acc tta gtc tca tca cca ccg aaa ctc cga cca gaa atg act			240
Asn His Thr Leu Val Ser Ser Pro Pro Lys Leu Arg Pro Glu Met Thr			
65	70	75	80
ctc gca aca gct ctc ttc acc acc gtc gaa gat gta atc aac acg ttc			288
Leu Ala Thr Ala Leu Phe Thr Thr Val Glu Asp Val Ile Asn Thr Phe			
85	90	95	
atc gat cca cct tca cgt cct tcc gtt gat cca aaa cat gtc ctc tct			336
Ile Asp Pro Pro Ser Arg Pro Ser Val Asp Pro Lys His Val Leu Ser			
100	105	110	
gat aac ttc gct cct gtc ctc gac gag ctt cct cca aca gac tgt gaa			384
Asp Asn Phe Ala Pro Val Leu Asp Glu Leu Pro Pro Thr Asp Cys Glu			
115	120	125	
atc atc cac ggc act ctt cca ctg tca ctt aac ggc gct tac atc cgt			432
Ile Ile His Gly Thr Leu Pro Leu Ser Leu Asn Gly Ala Tyr Ile Arg			
130	135	140	
aac ggt cca aat cca cag ttt ctc cct cgt ggt cct tac cat ctc ttc			480
Asn Gly Pro Asn Pro Gln Phe Leu Pro Arg Gly Pro Tyr His Leu Phe			
145	150	155	160
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Asp Gly Asp Gly Met Leu His Ala Ile Lys Ile His Asn Gly Lys Ala			
165	170	175	
act ctc tgt agc aga tac gtc aag act tat aaa tac aac gtc gag aaa			576
Thr Leu Cys Ser Arg Tyr Val Lys Thr Tyr Lys Tyr Asn Val Glu Lys			
180	185	190	
caa acc gga gct ccg gtt atg cct aac gtg ttt tcc gga ttc aac ggt			624
Gln Thr Gly Ala Pro Val Met Pro Asn Val Phe Ser Gly Phe Asn Gly			
195	200	205	
gta acg gcg tca gta gct cgt gga gct tta acg gca gct agg gtt tta			672
Val Thr Ala Ser Val Ala Arg Gly Ala Leu Thr Ala Ala Arg Val Leu			

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Thr Gly Gln Tyr Asn Pro Val Asn Gly Ile Gly Leu Ala Asn Thr Ser			
225	230	235	240
cta gct ttc ttc agt aac cgt ctc ttt gct tta ggt gaa tct gat tta	768		
Leu Ala Phe Phe Ser Asn Arg Leu Phe Ala Leu Gly Glu Ser Asp Leu			
245	250	255	
ccc tac gcc gtc cga tta acc gaa tca gga gat att gaa acg atc gga	816		
Pro Tyr Ala Val Arg Leu Thr Glu Ser Gly Asp Ile Glu Thr Ile Gly			
260	265	270	
cgg tac gat ttc gac ggg aaa tta gcg atg agt atg aca gct cat cct	864		
Arg Tyr Asp Phe Asp Gly Lys Leu Ala Met Ser Met Thr Ala His Pro			
275	280	285	
aaa acc gat cca ata acc gga gaa act ttc gct ttc cgg tac ggt ccg	912		
Lys Thr Asp Pro Ile Thr Gly Glu Thr Phe Ala Phe Arg Tyr Gly Pro			
290	295	300	
gtt cca ccg ttt tta aca tat ttc cgg ttt gat tcc gcc ggg aaa aaa	960		
Val Pro Pro Phe Leu Thr Tyr Phe Arg Phe Asp Ser Ala Gly Lys Lys			
305	310	315	320
caa aga gac gtt ccg ata ttc tcg atg acg tct ccg tcg ttt ctc cat	1008		
Gln Arg Asp Val Pro Ile Phe Ser Met Thr Ser Pro Ser Phe Leu His			
325	330	335	
gac ttc gcg atc acg aaa cgt cac gcg att ttc gca gag att cag ctt	1056		
Asp Phe Ala Ile Thr Lys Arg His Ala Ile Phe Ala Glu Ile Gln Leu			
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ggc atg agg atg aac atg ttg gat ttg gtt ctc gaa ggt ggt tct ccg	1104		
Gly Met Arg Met Asn Met Leu Asp Leu Val Leu Glu Gly Gly Ser Pro			
355	360	365	
gtt ggt act gat aac gga aaa act cca agg ctt gga gtg att cct aag	1152		
Val Gly Thr Asp Asn Gly Lys Thr Pro Arg Leu Gly Val Ile Pro Lys			





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Leu Ala Thr Ala Leu Phe Thr Thr Val Glu Asp Val Ile Asn Thr Phe  
85 90 95

Ile Asp Pro Pro Ser Arg Pro Ser Val Asp Pro Lys His Val Leu Ser  
100 105 110

Asp Asn Phe Ala Pro Val Leu Asp Glu Leu Pro Pro Thr Asp Cys Glu  
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Ile Ile His Gly Thr Leu Pro Leu Ser Leu Asn Gly Ala Tyr Ile Arg  
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Asn Gly Pro Asn Pro Gln Phe Leu Pro Arg Gly Pro Tyr His Leu Phe  
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Asp Gly Asp Gly Met Leu His Ala Ile Lys Ile His Asn Gly Lys Ala  
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Thr Leu Cys Ser Arg Tyr Val Lys Thr Tyr Lys Tyr Asn Val Glu Lys  
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Gln Thr Gly Ala Pro Val Met Pro Asn Val Phe Ser Gly Phe Asn Gly  
195 200 205

Val Thr Ala Ser Val Ala Arg Gly Ala Leu Thr Ala Ala Arg Val Leu  
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Thr Gly Gln Tyr Asn Pro Val Asn Gly Ile Gly Leu Ala Asn Thr Ser  
225 230 235 240

Leu Ala Phe Phe Ser Asn Arg Leu Phe Ala Leu Gly Glu Ser Asp Leu  
245 250 255

Pro Tyr Ala Val Arg Leu Thr Glu Ser Gly Asp Ile Glu Thr Ile Gly  
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Arg Tyr Asp Phe Asp Gly Lys Leu Ala Met Ser Met Thr Ala His Pro  
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Lys Thr Asp Pro Ile Thr Gly Glu Thr Phe Ala Phe Arg Tyr Gly Pro

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Gln Arg Asp Val Pro Ile Phe Ser Met Thr Ser Pro Ser Phe Leu His		
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Asp Phe Ala Ile Thr Lys Arg His Ala Ile Phe Ala Glu Ile Gln Leu		
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Gly Met Arg Met Asn Met Leu Asp Leu Val Leu Glu Gly Gly Ser Pro		
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Val Gly Thr Asp Asn Gly Lys Thr Pro Arg Leu Gly Val Ile Pro Lys		
370	375	380
Tyr Ala Gly Asp Glu Ser Glu Met Lys Trp Phe Glu Val Pro Gly Phe		
385	390	395 400
Asn Ile Ile His Ala Ile Asn Ala Trp Asp Glu Asp Asp Gly Asn Ser		
405	410	415
Val Val Leu Ile Ala Pro Asn Ile Met Ser Ile Glu His Thr Leu Glu		
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Arg Met Asp Leu Val His Ala Leu Val Glu Lys Val Lys Ile Asp Leu		
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Val Thr Gly Ile Val Arg Arg His Pro Ile Ser Ala Arg Asn Leu Asp		
450	455	460
Phe Ala Val Ile Asn Pro Ala Phe Leu Gly Arg Cys Ser Arg Tyr Val		
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Tyr Ala Ala Ile Gly Asp Pro Met Pro Lys Ile Ser Gly Val Val Lys		
485	490	495
Leu Asp Val Ser Lys Gly Asp Arg Asp Asp Cys Thr Val Ala Arg Arg		
500	505	510

Met Tyr Gly Ser Gly Cys Tyr Gly Gly Glu Pro Phe Phe Val Ala Arg  
 515 520 525

Asp Pro Gly Asn Pro Glu Ala Glu Glu Asp Asp Gly Tyr Val Val Thr  
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Tyr Val His Asp Glu Val Thr Gly Glu Ser Lys Phe Leu Val Met Asp  
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Ala Lys Ser Pro Glu Leu Glu Ile Val Ala Ala Val Arg Leu Pro Arg  
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 Ser Tyr Cys Ser Ser Leu Pro Met Ala Ser Arg Val Thr Arg Lys Leu





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Val Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Thr Gly Ile Ala			
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cga ctc atg cta ttc tac gcc aga gct gca gcc ggt ata gtc gac ccg			720
Arg Leu Met Leu Phe Tyr Ala Arg Ala Ala Gly Ile Val Asp Pro			
225	230	235	240
gca cac gga acc ggt gta gct aac gcc ggt ttg gtc tat ttc aat gcc			768
Ala His Gly Thr Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Gly			
245	250	255	
cgg tta ttg gct atg tcg gag gat gat tta cct tac caa gtt cag atc			816
Arg Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr Gln Val Gln Ile			
260	265	270	
act ccc aat gga gat tta aaa acc gtt ggt cgg ttc gat ttt gat gga			864
Thr Pro Asn Gly Asp Leu Lys Thr Val Gly Arg Phe Asp Phe Asp Gly			
275	280	285	
caa tta gaa tcc aca atg att gcc cac ccg aaa gtc gac ccg gaa tcc			912
Gln Leu Glu Ser Thr Met Ile Ala His Pro Lys Val Asp Pro Glu Ser			
290	295	300	
ggt gaa ctc ttc gct tta agc tac gac gtc gtt tca aag cct tac cta			960
Gly Glu Leu Phe Ala Leu Ser Tyr Asp Val Val Ser Lys Pro Tyr Leu			
305	310	315	320
aaa tac ttc cga ttc tca ccg gac gga act aaa tca ccg gac gtc gag			1008
Lys Tyr Phe Arg Phe Ser Pro Asp Gly Thr Lys Ser Pro Asp Val Glu			
325	330	335	
att cag ctt gat cag cca acg atg atg cac gat ttc gcg att aca gag			1056
Ile Gln Leu Asp Gln Pro Thr Met Met His Asp Phe Ala Ile Thr Glu			
340	345	350	
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Arg Phe Gly Ile Leu Asp Lys Tyr Ala Glu Asp Ser Ser Asn Ile Lys			
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tgg att gat gct cca gat tgc ttc tgc ttc cat ctc tgg aac gct tgg			1248
Trp Ile Asp Ala Pro Asp Cys Phe Cys Phe His Leu Trp Asn Ala Trp			
405	410	415	
gaa gag cca gaa aca gat gaa gtc gtc gtg ata ggg tcc tgt atg act			1296
Glu Glu Pro Glu Thr Asp Glu Val Val Val Ile Gly Ser Cys Met Thr			
420	425	430	
cca cca gac tca att ttc aac gag tct gac gag aat ctc aag agt gtc			1344
Pro Pro Asp Ser Ile Phe Asn Glu Ser Asp Glu Asn Leu Lys Ser Val			
435	440	445	
ctg tct gaa atc cgc ctg aat ctc aaa acc ggt gaa tca act cgc cgt			1392
Leu Ser Glu Ile Arg Leu Asn Leu Lys Thr Gly Glu Ser Thr Arg Arg			
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ccg atc atc tcc aac gaa gat caa caa gtc aac ctc gaa gca ggg atg			1440
Pro Ile Ile Ser Asn Glu Asp Gln Gln Val Asn Leu Glu Ala Gly Met			
465	470	475	480
gtc aac aga aac atg ctc ggc cgt aaa acc aaa ttc gct tac ttg gct			1488
Val Asn Arg Asn Met Leu Gly Arg Lys Thr Lys Phe Ala Tyr Leu Ala			
485	490	495	
tta gcc gag ccg tgg cct aaa gtc tca gga ttc gct aaa gtt gat ctc			1536
Leu Ala Glu Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu			
500	505	510	
act act gga gaa gtt aag aaa cat ctt tac ggc gat aac cgt tac gga			1584
Thr Thr Gly Glu Val Lys Lys His Leu Tyr Gly Asp Asn Arg Tyr Gly			







485                      490                      495  
 Leu Ala Glu Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu  
                     500                      505                      510  
 Thr Thr Gly Glu Val Lys Lys His Leu Tyr Gly Asp Asn Arg Tyr Gly  
                     515                      520                      525  
 Gly Glu Pro Leu Phe Leu Pro Gly Glu Gly Gly Glu Glu Asp Glu Gly  
                     530                      535                      540  
 Tyr Ile Leu Cys Phe Val His Asp Glu Lys Thr Trp Lys Ser Glu Leu  
 545                      550                      555                      560  
 Gln Ile Val Asn Ala Val Ser Leu Glu Val Glu Ala Thr Val Lys Leu  
                     565                      570                      575  
 Pro Ser Arg Val Pro Tyr Gly Phe His Gly Thr Phe Ile Gly Ala Asp  
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 Asp Leu Ala Lys Gln Val Val  
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&lt;211&gt; 1617

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

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atg gcg gag aaa ctc agt gat ggc agc agc atc atc tca gtc cat cct    48  
 Met Ala Glu Lys Leu Ser Asp Gly Ser Ser Ile Ile Ser Val His Pro  
       1                      5                      10                      15

aga ccc tcc aag ggt ttc tcc tcg aag ctt ctc gat ctt ctc gag aga    96  
 Arg Pro Ser Lys Gly Phe Ser Ser Lys Leu Leu Asp Leu Leu Glu Arg

20	25	30	
ctt gtt gtc aag ctc atg cac gat gct tct ctc cct ctc cac tac ctc			144
Leu Val Val Lys Leu Met His Asp Ala Ser Leu Pro Leu His Tyr Leu			
35	40	45	
tca ggc aac ttc gct ccc atc cgt gat gaa act cct ccc gtc aag gat			192
Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp			
50	55	60	
ctc ccc gtc cat gga ttt ctt ccc gaa tgc ttg aat ggt gaa ttt gtg			240
Leu Pro Val His Gly Phe Leu Pro Glu Cys Leu Asn Gly Glu Phe Val			
65	70	75	80
agg gtt ggt cca aac ccc aag ttt gat gct gtc gct gga tat cac tgg			288
Arg Val Gly Pro Asn Pro Lys Phe Asp Ala Val Ala Gly Tyr His Trp			
85	90	95	
ttt gat gga gat ggg atg att cat ggg gta cgc atc aaa gat ggg aaa			336
Phe Asp Gly Asp Gly Met Ile His Gly Val Arg Ile Lys Asp Gly Lys			
100	105	110	
gct act tat gtt tct cga tat gtt aag aca tca cgt ctt aag cag gaa			384
Ala Thr Tyr Val Ser Arg Tyr Val Lys Thr Ser Arg Leu Lys Gln Glu			
115	120	125	
gag ttc ttc gga gct gcc aaa ttc atg aag att ggt gac ctt aag ggg			432
Glu Phe Phe Gly Ala Ala Lys Phe Met Lys Ile Gly Asp Leu Lys Gly			
130	135	140	
ttt ttc gga ttg cta atg gtc aat gtc caa cag ctg aga acg aag ctc			480
Phe Phe Gly Leu Leu Met Val Asn Val Gln Gln Leu Arg Thr Lys Leu			
145	150	155	160
aaa ata ttg gac aac act tat gga aat gga act gcc aat aca gca ctc			528
Lys Ile Leu Asp Asn Thr Tyr Gly Asn Gly Thr Ala Asn Thr Ala Leu			
165	170	175	
gta tat cac cat gga aaa ctt cta gca tta cag gag gca gat aag ccg			576
Val Tyr His His Gly Lys Leu Leu Ala Leu Gln Glu Ala Asp Lys Pro			

180					185					190						
tac	gtc	atc	aaa	gtt	ttg	gaa	gat	gga	gac	ctg	caa	act	ctt	ggt	ata	624
Tyr	Val	Ile	Lys	Val	Leu	Glu	Asp	Gly	Asp	Leu	Gln	Thr	Leu	Gly	Ile	
195					200					205						
ata	gat	tat	gac	aag	aga	ttg	acc	cac	tcc	ttc	act	gct	cac	cca	aaa	672
Ile	Asp	Tyr	Asp	Lys	Arg	Leu	Thr	His	Ser	Phe	Thr	Ala	His	Pro	Lys	
210					215					220						
gtt	gac	ccg	gtt	acg	ggc	gaa	atg	ttt	aca	ttc	ggc	tat	tgc	cat	acg	720
Val	Asp	Pro	Val	Thr	Gly	Glu	Met	Phe	Thr	Phe	Gly	Tyr	Ser	His	Thr	
225					230					235					240	
cca	cct	tat	ctc	aca	tac	aga	gtt	atc	tgc	aaa	gat	ggc	att	atg	cat	768
Pro	Pro	Tyr	Leu	Thr	Tyr	Arg	Val	Ile	Ser	Lys	Asp	Gly	Ile	Met	His	
245					250					255						
gac	cca	gtc	cca	att	act	ata	tca	gag	cct	atc	atg	atg	cat	gat	ttt	816
Asp	Pro	Val	Pro	Ile	Thr	Ile	Ser	Glu	Pro	Ile	Met	Met	His	Asp	Phe	
260					265					270						
gct	att	act	gag	act	tat	gca	atc	ttc	atg	gat	ctt	cct	atg	cac	ttc	864
Ala	Ile	Thr	Glu	Thr	Tyr	Ala	Ile	Phe	Met	Asp	Leu	Pro	Met	His	Phe	
275					280					285						
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Arg	Pro	Lys	Glu	Met	Val	Lys	Glu	Lys	Lys	Met	Ile	Tyr	Ser	Phe	Asp	
290					295					300						
ccc	aca	aaa	aag	gct	cgt	ttt	ggc	gtt	ctt	cca	cgc	tat	gcc	aag	gat	960
Pro	Thr	Lys	Lys	Ala	Arg	Phe	Gly	Val	Leu	Pro	Arg	Tyr	Ala	Lys	Asp	
305					310					315					320	
gaa	ctt	atg	att	aga	tgg	ttt	gag	ctt	ccc	aac	tgc	ttt	att	ttc	cac	1008
Glu	Leu	Met	Ile	Arg	Trp	Phe	Glu	Leu	Pro	Asn	Cys	Phe	Ile	Phe	His	
325					330					335						
aac	gcc	aat	gct	tgg	gaa	gaa	gag	gat	gaa	gtc	gtc	ctc	atc	act	tgt	1056
Asn	Ala	Asn	Ala	Trp	Glu	Glu	Glu	Asp	Glu	Val	Val	Leu	Ile	Thr	Cys	



340	345	350	
cg t ctt gag aat cca gat ctt gac atg gtc agt ggg aaa gtg aaa gaa			1104
Arg Leu Glu Asn Pro Asp Leu Asp Met Val Ser Gly Lys Val Lys Glu			
355	360	365	
aaa ctc gaa aat ttt ggc aac gaa ctg tac gaa atg aga ttc aac atg			1152
Lys Leu Glu Asn Phe Gly Asn Glu Leu Tyr Glu Met Arg Phe Asn Met			
370	375	380	
aaa acg ggc tca gct tct caa aaa aaa cta tcc gca tct gcg gtt gat			1200
Lys Thr Gly Ser Ala Ser Gln Lys Lys Leu Ser Ala Ser Ala Val Asp			
385	390	395	400
ttc ccc aga atc aat gag tgc tac acc gga aag aaa cag aga tac gta			1248
Phe Pro Arg Ile Asn Glu Cys Tyr Thr Gly Lys Lys Gln Arg Tyr Val			
405	410	415	
tat gga aca att ctg gac agt atc gca aag gtt acc gga atc atc aag			1296
Tyr Gly Thr Ile Leu Asp Ser Ile Ala Lys Val Thr Gly Ile Ile Lys			
420	425	430	
ttt gat ctg cat gca gaa gct gag aca ggg aaa aga atg ctg gaa gta			1344
Phe Asp Leu His Ala Glu Ala Glu Thr Gly Lys Arg Met Leu Glu Val			
435	440	445	
gga ggt aat atc aaa gga ata tat gac ctg gga gaa ggc aga tat ggt			1392
Gly Gly Asn Ile Lys Gly Ile Tyr Asp Leu Gly Glu Gly Arg Tyr Gly			
450	455	460	
tca gag gct atc tat gtt ccg cgt gag aca gca gaa gaa gac gac ggt			1440
Ser Glu Ala Ile Tyr Val Pro Arg Glu Thr Ala Glu Glu Asp Asp Gly			
465	470	475	480
tac ttg ata ttc ttt gtt cat gat gaa aac aca ggg aaa tca tgc gtg			1488
Tyr Leu Ile Phe Phe Val His Asp Glu Asn Thr Gly Lys Ser Cys Val			
485	490	495	
act gtg ata gac gca aaa aca atg tcg gct gaa ccg gtg gca gtg gtg			1536
Thr Val Ile Asp Ala Lys Thr Met Ser Ala Glu Pro Val Ala Val Val			

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500

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gag ctg ccg cac agg gtc cca tat ggc ttc cat gcc ttg ttt gtt aca 1584

Glu Leu Pro His Arg Val Pro Tyr Gly Phe His Ala Leu Phe Val Thr

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525

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1617

Glu Glu Gln Leu Gln Glu Gln Thr Leu Ile

530

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<211> 538

<212> PRT

<213> Arabidopsis thaliana

<400> 8

Met Ala Glu Lys Leu Ser Asp Gly Ser Ser Ile Ile Ser Val His Pro

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Arg Pro Ser Lys Gly Phe Ser Ser Lys Leu Leu Asp Leu Leu Glu Arg

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Leu Val Val Lys Leu Met His Asp Ala Ser Leu Pro Leu His Tyr Leu

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Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp

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Leu Pro Val His Gly Phe Leu Pro Glu Cys Leu Asn Gly Glu Phe Val

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Arg Val Gly Pro Asn Pro Lys Phe Asp Ala Val Ala Gly Tyr His Trp

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Phe Asp Gly Asp Gly Met Ile His Gly Val Arg Ile Lys Asp Gly Lys

100

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110

Ala Thr Tyr Val Ser Arg Tyr Val Lys Thr Ser Arg Leu Lys Gln Glu

115

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Glu Phe Phe Gly Ala Ala Lys Phe Met Lys Ile Gly Asp Leu Lys Gly  
130 135 140

Phe Phe Gly Leu Leu Met Val Asn Val Gln Gln Leu Arg Thr Lys Leu  
145 150 155 160

Lys Ile Leu Asp Asn Thr Tyr Gly Asn Gly Thr Ala Asn Thr Ala Leu  
165 170 175

Val Tyr His His Gly Lys Leu Leu Ala Leu Gln Glu Ala Asp Lys Pro  
180 185 190

Tyr Val Ile Lys Val Leu Glu Asp Gly Asp Leu Gln Thr Leu Gly Ile  
195 200 205

Ile Asp Tyr Asp Lys Arg Leu Thr His Ser Phe Thr Ala His Pro Lys  
210 215 220

Val Asp Pro Val Thr Gly Glu Met Phe Thr Phe Gly Tyr Ser His Thr  
225 230 235 240

Pro Pro Tyr Leu Thr Tyr Arg Val Ile Ser Lys Asp Gly Ile Met His  
245 250 255

Asp Pro Val Pro Ile Thr Ile Ser Glu Pro Ile Met Met His Asp Phe  
260 265 270

Ala Ile Thr Glu Thr Tyr Ala Ile Phe Met Asp Leu Pro Met His Phe  
275 280 285

Arg Pro Lys Glu Met Val Lys Glu Lys Lys Met Ile Tyr Ser Phe Asp  
290 295 300

Pro Thr Lys Lys Ala Arg Phe Gly Val Leu Pro Arg Tyr Ala Lys Asp  
305 310 315 320

Glu Leu Met Ile Arg Trp Phe Glu Leu Pro Asn Cys Phe Ile Phe His  
325 330 335

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435	440	445	
gta acc gga gtg aat tta gaa gcg ggt cac ata aac cgt agt tac gtg			1392
Val Thr Gly Val Asn Leu Glu Ala Gly His Ile Asn Arg Ser Tyr Val			
450	455	460	
ggc cgg aaa agc cag ttc gtt tac ata gca ata gcc gat cct tgg ccc			1440
Gly Arg Lys Ser Gln Phe Val Tyr Ile Ala Ile Ala Asp Pro Trp Pro			
465	470	475	480
aaa tgc agt ggc att gcg aag gta gat ata caa aac ggc acc gtt tca			1488
Lys Cys Ser Gly Ile Ala Lys Val Asp Ile Gln Asn Gly Thr Val Ser			
485	490	495	
gag ttt aat tac gga ccg agc cgg ttc ggt gga gaa ccg tgc ttt gta			1536
Glu Phe Asn Tyr Gly Pro Ser Arg Phe Gly Gly Glu Pro Cys Phe Val			
500	505	510	
ccg gag gga gaa gga gaa gaa gac aaa ggt tat gta atg ggg ttt gtg			1584
Pro Glu Gly Glu Gly Glu Glu Asp Lys Gly Tyr Val Met Gly Phe Val			
515	520	525	
aga gac gaa gag aaa gac gag tcg gag ttt gtg gtg gtc gac gcg acg			1632
Arg Asp Glu Glu Lys Asp Glu Ser Glu Phe Val Val Val Asp Ala Thr			
530	535	540	
gat atg aag caa gtc gcg gcg gtg cgc ttg ccg gag agg gta cct tat			1680
Asp Met Lys Gln Val Ala Ala Val Arg Leu Pro Glu Arg Val Pro Tyr			
545	550	555	560
ggt ttc cat gga acg ttc gtg agc gag aat cag ttg aag gaa caa gtt			1728
Gly Phe His Gly Thr Phe Val Ser Glu Asn Gln Leu Lys Glu Gln Val			
565	570	575	
ttc tga			1734
Phe			

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&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 10

Met	Gln	His	Ser	Leu	Arg	Ser	Asp	Leu	Leu	Pro	Thr	Lys	Thr	Ser	Pro
1				5					10					15	

Arg	Ser	His	Leu	Leu	Pro	Gln	Pro	Lys	Asn	Ala	Asn	Ile	Ser	Arg	Arg
			20					25					30		

Ile	Leu	Ile	Asn	Pro	Phe	Lys	Ile	Pro	Thr	Leu	Pro	Asp	Leu	Thr	Ser
			35				40					45			

Pro	Val	Pro	Ser	Pro	Val	Lys	Leu	Lys	Pro	Thr	Tyr	Pro	Asn	Leu	Asn
			50			55					60				

Leu	Leu	Gln	Lys	Leu	Ala	Ala	Thr	Met	Leu	Asp	Lys	Ile	Glu	Ser	Ser
65					70					75				80	

Ile	Val	Ile	Pro	Met	Glu	Gln	Asn	Arg	Pro	Leu	Pro	Lys	Pro	Thr	Asp
				85					90					95	

Pro	Ala	Val	Gln	Leu	Ser	Gly	Asn	Phe	Ala	Pro	Val	Asn	Glu	Cys	Pro
			100					105					110		

Val	Gln	Asn	Gly	Leu	Glu	Val	Val	Gly	Gln	Ile	Pro	Ser	Cys	Leu	Lys
			115					120					125		

Gly	Val	Tyr	Ile	Arg	Asn	Gly	Ala	Asn	Pro	Met	Phe	Pro	Pro	Leu	Ala
		130				135					140				

Gly	His	His	Leu	Phe	Asp	Gly	Asp	Gly	Met	Ile	His	Ala	Val	Ser	Ile
145					150				155					160	

Gly	Phe	Asp	Asn	Gln	Val	Ser	Tyr	Ser	Cys	Arg	Tyr	Thr	Lys	Thr	Asn
			165						170					175	

Arg	Leu	Val	Gln	Glu	Thr	Ala	Leu	Gly	Arg	Ser	Val	Phe	Pro	Lys	Pro
			180					185						190	

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Ile Gly Glu Leu His Gly His Ser Gly Leu Ala Arg Leu Ala Leu Phe  
195 200 205

Thr Ala Arg Ala Gly Ile Gly Leu Val Asp Gly Thr Arg Gly Met Gly  
210 215 220

Val Ala Asn Ala Gly Val Val Phe Phe Asn Gly Arg Leu Leu Ala Met  
225 230 235 240

Ser Glu Asp Asp Leu Pro Tyr Gln Val Lys Ile Asp Gly Gln Gly Asp  
245 250 255

Leu Glu Thr Ile Gly Arg Phe Gly Phe Asp Asp Gln Ile Asp Ser Ser  
260 265 270

Val Ile Ala His Pro Lys Val Asp Ala Thr Thr Gly Asp Leu His Thr  
275 280 285

Leu Ser Tyr Asn Val Leu Lys Lys Pro His Leu Arg Tyr Leu Lys Phe  
290 295 300

Asn Thr Cys Gly Lys Lys Thr Arg Asp Val Glu Ile Thr Leu Pro Glu  
305 310 315 320

Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn Phe Val Val Ile  
325 330 335

Pro Asp Gln Gln Met Val Phe Lys Leu Ser Glu Met Ile Arg Gly Gly  
340 345 350

Ser Pro Val Ile Tyr Val Lys Glu Lys Met Ala Arg Phe Gly Val Leu  
355 360 365

Ser Lys Gln Asp Leu Thr Gly Ser Asp Ile Asn Trp Val Asp Val Pro  
370 375 380

Asp Cys Phe Cys Phe His Leu Trp Asn Ala Trp Glu Glu Arg Thr Glu  
385 390 395 400

Glu Gly Asp Pro Val Ile Val Val Ile Gly Ser Cys Met Ser Pro Pro

195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

405	410	415
Asp Thr Ile Phe Ser Glu Ser Gly Glu Pro Thr Arg Val Glu Leu Ser		
420	425	430
Glu Ile Arg Leu Asn Met Arg Thr Lys Glu Ser Asn Arg Lys Val Ile		
435	440	445
Val Thr Gly Val Asn Leu Glu Ala Gly His Ile Asn Arg Ser Tyr Val		
450	455	460
Gly Arg Lys Ser Gln Phe Val Tyr Ile Ala Ile Ala Asp Pro Trp Pro		
465	470	475
Lys Cys Ser Gly Ile Ala Lys Val Asp Ile Gln Asn Gly Thr Val Ser		
485	490	495
Glu Phe Asn Tyr Gly Pro Ser Arg Phe Gly Gly Glu Pro Cys Phe Val		
500	505	510
Pro Glu Gly Glu Gly Glu Glu Asp Lys Gly Tyr Val Met Gly Phe Val		
515	520	525
Arg Asp Glu Glu Lys Asp Glu Ser Glu Phe Val Val Val Asp Ala Thr		
530	535	540
Asp Met Lys Gln Val Ala Ala Val Arg Leu Pro Glu Arg Val Pro Tyr		
545	550	555
Gly Phe His Gly Thr Phe Val Ser Glu Asn Gln Leu Lys Glu Gln Val		
565	570	575

Phe

&lt;210&gt; 11

&lt;211&gt; 1839

&lt;212&gt; DNA

&lt;213&gt; Vigna unguiculata

T 693463

**<220>**

<222> (1)..(1839)

atg cct tca tca gct tca aac act tgg ttt aac gcc aca ctc cca tct 48  
Met Pro Ser Ser Ala Ser Asn Thr Trp Phe Asn Ala Thr Leu Pro Ser  
1 5 10 15







<210> 12

<212> PRT

<400> 12

Pro Pro Phe Lys Asp Leu Pro Ser Thr Ser Ser Pro Thr Asn Leu Leu  
20 25 30

Pro Leu Arg Lys Thr Ser Ser Ser Asn Thr Ile Thr Cys Ser Leu Gln  
35 40 45

Thr Leu His Phe Pro Lys Gln Tyr Gln Pro Thr Ser Thr Ser Thr Ser  
50 55 60

Thr Ala Thr Thr Thr Thr Pro Thr Pro Ile Lys Thr Thr Thr Ile Thr  
65 70 75 80

Thr Thr Thr Pro Pro Arg Glu Thr Asn Pro Leu Ser Asp Thr Asn Gln  
85 90 95

Pro Leu Pro Gln Lys Trp Asn Phe Leu Gln Lys Ala Ala Ala Thr Ala  
100 105 110

Leu Asp Leu Val Glu Thr Ala Leu Val Ser His Glu Arg Lys His Pro  
115 120 125

Leu Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Phe Ala  
130 135 140

Pro Val Pro Glu His Ala Ala Asp Gln Gly Leu Pro Val Val Gly Lys  
145                      150                      155                      160

Ile Pro Lys Cys Ile Asp Gly Val Tyr Val Arg Asn Gly Ala Asn Pro  
165 170 175







605

aag aag cag ctc aac ttg ttc cag cgc gcc gcg gcg gcc gcg ctc gac 288  
Lys Lys Gln Leu Asn Leu Phe Gln Arg Ala Ala Ala Ala Ala Leu Asp  
85 90 95

ccc tgg gcc ggc acc ggc gtg gcc aac gcc ggc ctc gtc tac ttc aac 768  
Pro Ser Ala Gly Thr Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn  
245 250 255





gcc acg gtt cag ctg ccg tcc cgc gtg ccc ttc ggc ttc cac ggc acc 1776  
 Ala Thr Val Gln Leu Pro Ser Arg Val Pro Phe Gly Phe His Gly Thr  
                   580                  585                  590

ttc atc acg ggc cag gag ctc gag gcc cag gcg gcc tga 1815  
 Phe Ile Thr Gly Gln Glu Leu Glu Ala Gln Ala Ala  
                   595                  600                  605

<210> 14

<211> 604

<212> PRT

<213> Zea mays

<400> 14

Met Gln Gly Leu Ala Pro Pro Thr Ser Val Ser Ile His Arg His Leu  
       1                  5                  10                  15

Pro Ala Arg Ser Arg Ala Arg Ala Ser Asn Ser Val Arg Phe Ser Pro  
                   20                  25                  30

Arg Ala Val Ser Ser Val Pro Pro Ala Glu Cys Leu Gln Ala Pro Phe  
                   35                  40                  45

His Lys Pro Val Ala Asp Leu Pro Ala Pro Ser Arg Lys Pro Ala Ala  
                   50                  55                  60

Ile Ala Val Pro Gly His Ala Ala Ala Pro Arg Lys Ala Glu Gly Gly  
       65                  70                  75                  80

Lys Lys Gln Leu Asn Leu Phe Gln Arg Ala Ala Ala Ala Leu Asp  
                   85                  90                  95

Ala Phe Glu Glu Gly Phe Val Ala Asn Val Leu Glu Arg Pro His Gly  
                   100                  105                  110

Leu Pro Ser Thr Ala Asp Pro Ala Val Gln Ile Ala Gly Asn Phe Ala  
                   115                  120                  125

Pro Val Gly Glu Arg Pro Pro Val His Glu Leu Pro Val Ser Gly Arg

1776-1815

130		135		140
Ile Pro Pro Phe Ile Asp Gly Val Tyr Ala Arg Asn Gly Ala Asn Pro				
145		150		155
				160
Cys Phe Asp Pro Val Ala Gly His His Leu Phe Asp Gly Asp Gly Met				
	165		170	175
Val His Ala Leu Arg Ile Arg Asn Gly Ala Ala Glu Ser Tyr Ala Cys				
	180		185	190
Arg Phe Thr Glu Thr Ala Arg Leu Arg Gln Glu Arg Ala Ile Gly Arg				
	195		200	205
Pro Val Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile				
	210		215	220
Ala Arg Leu Ala Leu Phe Tyr Ala Arg Ala Ala Cys Gly Leu Val Asp				
225		230		235
				240
Pro Ser Ala Gly Thr Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn				
	245		250	255
Gly Arg Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr His Val Arg				
	260		265	270
Val Ala Asp Asp Gly Asp Leu Glu Thr Val Gly Arg Tyr Asp Phe Asp				
	275		280	285
Gly Gln Leu Gly Cys Ala Met Ile Ala His Pro Lys Leu Asp Pro Ala				
	290		295	300
Thr Gly Glu Leu His Ala Leu Ser Tyr Asp Val Ile Lys Arg Pro Tyr				
305		310		315
				320
Leu Lys Tyr Phe Tyr Phe Arg Pro Asp Gly Thr Lys Ser Asp Asp Val				
	325		330	335
Glu Ile Pro Leu Glu Gln Pro Thr Met Ile His Asp Phe Ala Ile Thr				
	340		345	350













aaa gaa tgg aaa tca gaa ctg caa att gtt aac gca atg agt ttg aag 1728  
 Lys Glu Trp Lys Ser Glu Leu Gln Ile Val Asn Ala Met Ser Leu Lys  
                   565                                  570                                  575

ttg gag gca act gtg aag ctt cca tca aga gtt cct tat gga ttt cat 1776  
 Leu Glu Ala Thr Val Lys Leu Pro Ser Arg Val Pro Tyr Gly Phe His  
                   580                                  585                                  590

gga aca ttc ata aac gcc aat gat ttg gca aat cag gca tga 1818  
 Gly Thr Phe Ile Asn Ala Asn Asp Leu Ala Asn Gln Ala  
                   595                                  600                                  605

<210> 16

<211> 605

<212> PRT

<213> Lycopersicon esculentum

<400> 16

Met Ala Thr Thr Thr Ser His Ala Thr Asn Thr Trp Ile Lys Thr Lys  
   1                                  5                                  10                                  15

Leu Ser Met Pro Ser Ser Lys Glu Phe Gly Phe Ala Ser Asn Ser Ile  
                   20                                  25                                  30

Ser Leu Leu Lys Asn Gln His Asn Arg Gln Ser Leu Asn Ile Asn Ser  
                   35                                  40                                  45

Ser Leu Gln Ala Pro Pro Ile Leu His Phe Pro Lys Gln Ser Ser Asn  
                   50                                  55                                  60

Tyr Gln Thr Pro Lys Asn Asn Thr Ile Ser His Pro Lys Gln Glu Asn  
                   65                                  70                                  75                                  80

Asn Asn Ser Ser Ser Ser Ser Thr Ser Lys Trp Asn Leu Val Gln Lys  
                                   85                                  90                                  95

Ala Ala Ala Met Ala Leu Asp Ala Val Glu Ser Ala Leu Thr Lys His  
                   100                                  105                                  110

69395460







tca ggc aac ttc gct ccc atc cgt gat gaa act cct ccc gtc aag gat 192  
Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp  
50 55 60

ctc ccc gtc cat gga ttt ctt ccc gaa tgc ttg aat ggt gaa ttt gtg 240  
 Leu Pro Val His Gly Phe Leu Pro Glu Cys Leu Asn Gly Glu Phe Val  
 65 70 75 80

agg gtt ggt cca aac ccc aag ttt gat gct gtc gct gga tat cac tgg 288  
 Arg Val Gly Pro Asn Pro Lys Phe Asp Ala Val Ala Gly Tyr His Trp  
 85 90 95

ttt gat gga gat ggg atg att cat ggg gta cgc atc aaa gat ggg aaa 336  
 Phe Asp Gly Asp Gly Met Ile His Gly Val Arg Ile Lys Asp Gly Lys  
 100 105 110

gct act tat gtt tct cga tat gtt aag aca tca cgt ctt aag cag gaa 384  
 Ala Thr Tyr Val Ser Arg Tyr Val Lys Thr Ser Arg Leu Lys Gln Glu  
 115 120 125

gag ttc ttc gga gct gcc aaa ttc atg aag att ggt gac ctt aag ggg 432  
 Glu Phe Phe Gly Ala Ala Lys Phe Met Lys Ile Gly Asp Leu Lys Gly  
 130 135 140

ttt ttc gga ttg cta atg gtc aat atc caa cag ctg aga acg aag ctc 480  
 Phe Phe Gly Leu Leu Met Val Asn Ile Gln Gln Leu Arg Thr Lys Leu  
 145 150 155 160

aaa ata ttg gac aac act tat gga aat gga act gcc aat aca gca ctc 528  
 Lys Ile Leu Asp Asn Thr Tyr Gly Asn Gly Thr Ala Asn Thr Ala Leu  
 165 170 175

gta tat cac cat gga aaa ctt cta gca tta cag gag gca gat aag ccg 576  
 Val Tyr His His Gly Lys Leu Leu Ala Leu Gln Glu Ala Asp Lys Pro  
 180 185 190

tac gtc atc aaa gtt ttg gaa gat gga gac ctg caa act ctt ggt ata 624  
 Tyr Val Ile Lys Val Leu Glu Asp Gly Asp Leu Gln Thr Leu Gly Ile  
 195 200 205

ata gat tat gac aag aga ttg acc cac tcc ttc act gct cac cca aaa 672  
 Ile Asp Tyr Asp Lys Arg Leu Thr His Ser Phe Thr Ala His Pro Lys  
 210 215 220



gag gaa caa ctc cag gaa caa act ctt ata taa 1617  
Glu Glu Gln Leu Gln Glu Gln Thr Leu Ile  
530 535

61/68

<210> 18

<211> 538

<212> PRT

<213> Arabidopsis thaliana

<400> 18

Met Ala Glu Lys Leu Ser Asp Gly Ser Ile Ile Ile Ser Val His Pro  
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Arg Pro Ser Lys Gly Phe Ser Ser Lys Leu Leu Asp Leu Leu Glu Arg  
20 25 30

Leu Val Val Lys Leu Met His Asp Ala Ser Leu Pro Leu His Tyr Leu  
35 40 45

Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp  
50 55 60

Leu Pro Val His Gly Phe Leu Pro Glu Cys Leu Asn Gly Glu Phe Val  
65 70 75 80

Arg Val Gly Pro Asn Pro Lys Phe Asp Ala Val Ala Gly Tyr His Trp  
85 90 95

Phe Asp Gly Asp Gly Met Ile His Gly Val Arg Ile Lys Asp Gly Lys  
100 105 110

Ala Thr Tyr Val Ser Arg Tyr Val Lys Thr Ser Arg Leu Lys Gln Glu  
115 120 125

Glu Phe Phe Gly Ala Ala Lys Phe Met Lys Ile Gly Asp Leu Lys Gly  
130 135 140

Phe Phe Gly Leu Leu Met Val Asn Ile Gln Gln Leu Arg Thr Lys Leu  
145 150 155 160

Lys Ile Leu Asp Asn Thr Tyr Gly Asn Gly Thr Ala Asn Thr Ala Leu  
165 170 175

Val Tyr His His Gly Lys Leu Leu Ala Leu Gln Glu Ala Asp Lys Pro  
 180 185 190

Tyr Val Ile Lys Val Leu Glu Asp Gly Asp Leu Gln Thr Leu Gly Ile  
 195 200 205

Ile Asp Tyr Asp Lys Arg Leu Thr His Ser Phe Thr Ala His Pro Lys  
 210 215 220

Val Asp Pro Val Thr Gly Glu Met Phe Thr Phe Gly Tyr Ser His Thr  
 225 230 235 240

Pro Pro Tyr Leu Thr Tyr Arg Val Ile Ser Lys Asp Gly Ile Met His  
 245 250 255

Asp Pro Val Pro Ile Thr Ile Ser Glu Pro Ile Met Met His Asp Phe  
 260 265 270

Ala Ile Thr Glu Thr Tyr Ala Ile Phe Met Asp Leu Pro Met His Phe  
 275 280 285

Arg Pro Lys Glu Met Val Lys Glu Lys Lys Met Ile Tyr Ser Phe Asp  
 290 295 300

Pro Thr Lys Lys Ala Arg Phe Gly Val Leu Pro Arg Tyr Ala Lys Asp  
 305 310 315 320

Glu Leu Met Ile Arg Trp Phe Glu Leu Pro Asn Cys Phe Ile Phe His  
 325 330 335

Asn Ala Asn Ala Trp Glu Glu Glu Asp Glu Val Val Leu Ile Thr Cys  
 340 345 350

Arg Leu Glu Asn Pro Asp Leu Asp Met Val Ser Gly Lys Val Lys Glu  
 355 360 365

Lys Leu Glu Asn Phe Gly Asn Glu Leu Tyr Glu Met Arg Phe Asn Met  
 370 375 380

Lys Thr Gly Ser Ala Ser Gln Lys Lys Leu Ser Ala Ser Ala Val Asp

69295459



attgaattca tgccttcagc ttcaaac

27

<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 20

attggatccc aaaagctaca cgctggtccc c

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<210> 21

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 21

atatatctag aatgccttca tcagcttcaa acacttgg

38

<210> 22

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 22

atataggatc cctccggcac cggcggaag ttcccc

36

64/68



<210> 23  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 23  
 cccgggatcc ctcaagcctc tctataccg

29

<210> 24  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 24  
 cccgggatcc tttatacgga ttctgaggga g

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<210> 25  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 25  
 attgaattca tggactctgt ttcttcttct tcc

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65/68  
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 33

**<210> 26**

**<212> DNA**

**<220>**

<400> 26

<210> 27

<212> DNA

**<220>**

**<400> 27**

<210> 28

## <212> DNA

**<220>**

<400> 28



<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 32

gttttcccag tcacgac

17

68/68 68/68 68/68